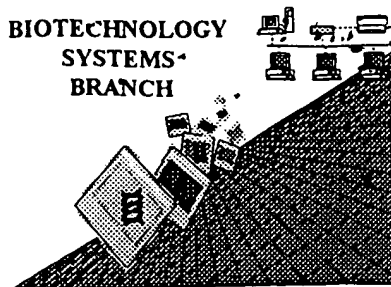


05711
0925

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09933115

Source: OIPE

Date Processed by STIC: 09/10/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09 933 175

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length. Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 ✓ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/933,115

DATE: 09/10/2001

TIME: 09:22:00

Input Set : A:\FISHERSEQLIST.TXT

Output Set: N:\CRF3\09102001\I933115.raw

Does Not Comply
Corrected Diskette Needed

See Page 6 of 7A

4 <110> APPLICANT: Fisher, Paul B.
 6 <120> TITLE OF INVENTION: COMBINATORIAL METHODS FOR INDUCING
 7 CANCER CELLS
 9 <130> FILE REFERENCE: a34466 070050.1618

C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/933,115

12 <141> CURRENT FILING DATE: 2001-08-20

14 <160> NUMBER OF SEQ ID NOS: 17

16 <170> SOFTWARE: FastSEQ for Windows Version 4.0

18 <210> SEQ ID NO: 1

19 <211> LENGTH: 1700

20 <212> TYPE: DNA

21 <213> ORGANISM: Homo sapiens

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24 <221> NAME/KEY: misc_feature

25 <222> LOCATION: (275)...(895)

26 <223> OTHER INFORMATION: CDS = 275-895

28 <400> SEQUENCE: 1

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 31 aaccagctgc ctccaggcag ccagccctca agcatcactt acaggaccag agggacaaga 180
 32 catgactgtg atgaggagct gctttcgcca atttaacacc aagaagaatt gaggtgctt 240
 33 gggaggaagg ccaggaggaa cagcagactg agagatgaat tttcaacaga ggctgcaaag 300
 34 cctgtggact ttagccagac ccttctgccc tcctttgtg ggcagagcct ctcaaagca 360
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 36 ccagggccaa gaattccact ttgggcccctg ccaagtgaag ggggttggtc ccagaaact 480
 37 gtgggaagcc ttctgggctg tgaaagacac tatgcaagct caggataaca tcacgagtgc 540
 38 ccggctgctg cagcaggagg ttctgcagaa cgtctcggat gctgagagct gttaccttgt 600
 39 ccacacctg ctggagttct acttgaaaac tgttttcaaa aactaccaca atagaacagt 660
 40 tgaagtcagg actctgaagt cattctctac tctggccaac aactttgttc tcatcggtgc 720
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 42 gtttctgcta ttccggagag cattcaaaca gttggacgta gaagcagctc tgaccaaagc 840
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 54 acatttcatt tcccaccac actcgccagc tcaccccatc atccctttcc cttggtgccc 1560
 55 tccttttttt tttatcctag tcattcttcc ctaatcttcc acttgagtgt caagctgacc 1620
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 57 ataaaagaca acataactca 1700

59 <210> SEQ ID NO: 2

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

check
diskette

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/933,115

TIME: 09:22:00

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Output Set: N:\CRF3\09102001\I933115.raw

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66 1 5 10 15
67 Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met Val Val
68 20 25 30
69 Leu Pro Cys Leu Gly Phe Thr Leu Leu Trp Ser Gln Val Ser Gly
70 35 40 45
71 Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln Val Lys Gly Val
72 50 55 60
73 Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala Val Lys Asp Thr Met
74 65 70 75 80
75 Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg Leu Leu Gln Gln Glu Val
76 85 90 95
77 Leu Gln Asn Val Ser Asp Ala Glu Ser Cys Tyr Leu Val His Thr Leu
78 100 105 110
79 Leu Glu Phe Tyr Leu Lys Thr Val Phe Lys Asn Tyr His Asn Arg Thr
80 115 120 125
81 Val Glu Val Arg Thr Leu Lys Ser Phe Ser Thr Leu Ala Asn Asn Phe
82 130 135 140
83 Val Leu Ile Val Ser Gln Leu Gln Pro Ser Gln Glu Asn Glu Met Phe
84 145 150 155 160
85 Ser Ile Arg Asp Ser Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala
86 165 170 175
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90 195 200 205
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96 <213> ORGANISM: Homo sapiens
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99 <221> NAME/KEY: misc_feature
100 <222> LOCATION: (0)...(0)
101 <223> OTHER INFORMATION: primer for mda-7
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106 <210> SEQ ID NO: 4
107 <211> LENGTH: 20
108 <212> TYPE: DNA
109 <213> ORGANISM: Homo sapiens
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113 <222> LOCATION: (0)...(0)
114 <223> OTHER INFORMATION: primer for MDA-7
116 <400> SEQUENCE: 4

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20

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/933,115

TIME: 09:22:00

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Output Set: N:\CRF3\09102001\I933115.raw

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122 <213> ORGANISM: Homo sapiens
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125 <223> OTHER INFORMATION: 153-164 of human MDA-7
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133 <211> LENGTH: 5775
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139 <222> LOCATION: (193)...(759)
140 <223> OTHER INFORMATION: CDS = 193-759
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145 cgcaggcact gaaggcggcg gcggggccag aggcctcagcg gctcccagggt gcgggagaga 180
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147 agtgccttga cgatacagct aattcagaat cattttgttg acgaatatga tccaacaata 300
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RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/933,115

TIME: 09:22:00

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RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/933,115

TIME: 09:22:00

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Output Set: N:\CRF3\09102001\I933115.raw

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252 35 40 45
253 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
254 50 55 60
255 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
256 65 70 75 80
257 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
258 85 90 95
259 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
260 100 105 110
261 Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
262 115 120 125
263 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
264 130 135 140
265 Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
266 145 150 155 160
267 Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
268 165 170 175
269 Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met
270 180 185
273 <210> SEQ ID NO: 8
274 <211> LENGTH: 188

```

09/933115

FISHERSEQLIST

Ser	Ala	Met	Arg	Asp	Gln	Tyr	Met	Arg	Thr	Gly	Glu	Gly	Phe	Leu	Cys
65					70					75					80
Val	Phe	Ala	Ile	Asn	Asn	Thr	Lys	Ser	Phe	Glu	Asp	Ile	His	His	Tyr
				85					90					95	
Arg	Glu	Gln	Ile	Lys	Arg	Val	Lys	Asp	Ser	Glu	Asp	Val	Pro	Met	Val
				100				105					110		
Leu	Val	Gly	Asn	Lys	Cys	Asp	Leu	Pro	Ser	Arg	Thr	Val	Asp	Thr	Lys
		115					120					125			
Gln	Ala	Gln	Asp	Leu	Ala	Arg	Ser	Tyr	Gly	Ile	Pro	Phe	Ile	Glu	Thr
	130					135					140				
Ser	Ala	Lys	Thr	Arg	Gln	Gly	Val	Asp	Asp	Ala	Phe	Tyr	Thr	Leu	Val
145					150					155					160
Arg	Glu	Ile	Arg	Lys	His	Lys	Glu	Lys	Met	Ser	Lys	Asp	Gly	Lys	Lys
				165					170					175	
Lys	Lys	Lys	Lys	Ser	Lys	Thr	Lys	Cys	Val	Ile	Met				
			180					185							

<210> 8
 <211> 188
 <212> PRT
 <213> Homo sapiens

Description of unknowns is
 required in fields 221, 222 and 223.

<220>
 <223> Xaa = any amino acid

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

<400> 8

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Xaa	Gly	Val	Gly	Lys
1				5					10					15	
Ser	Ala	Leu	Thr	Ile	Gln	Leu	Ile	Gln	Asn	His	Phe	Val	Asp	Glu	Tyr
			20					25					30		
Asp	Pro	Thr	Ile	Glu	Asp	Ser	Tyr	Arg	Lys	Gln	Val	Val	Ile	Asp	Gly
		35					40					45			
Glu	Thr	Cys	Leu	Leu	Asp	Ile	Leu	Asp	Thr	Ala	Gly	Gln	Glu	Glu	Tyr
	50				55					60					
Ser	Ala	Met	Arg	Asp	Gln	Tyr	Met	Arg	Thr	Gly	Glu	Gly	Phe	Leu	Cys
65					70					75					80
Val	Phe	Ala	Ile	Asn	Asn	Thr	Lys	Ser	Phe	Glu	Asp	Ile	His	His	Tyr
				85					90				95		
Arg	Glu	Gln	Ile	Lys	Arg	Val	Lys	Asp	Ser	Glu	Asp	Val	Pro	Met	Val
			100					105					110		
Leu	Val	Gly	Asn	Lys	Cys	Asp	Leu	Pro	Ser	Arg	Thr	Val	Asp	Thr	Lys
		115					120					125			
Gln	Ala	Gln	Asp	Leu	Ala	Arg	Ser	Tyr	Gly	Ile	Pro	Phe	Ile	Glu	Thr
	130					135					140				
Ser	Ala	Lys	Thr	Arg	Gln	Gly	Val	Asp	Asp	Ala	Phe	Tyr	Thr	Leu	Val
145					150					155					160
Arg	Glu	Ile	Arg	Lys	His	Lys	Glu	Lys	Met	Ser	Lys	Asp	Gly	Lys	Lys
				165					170					175	
Lys	Lys	Lys	Lys	Ser	Lys	Thr	Lys	Cys	Val	Ile	Met				
			180					185							

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

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 the Sequence Listing. Please check subsequent
 sequences for similar errors.

VERIFICATION SUMMARY

DATE: 09/10/2001

PATENT APPLICATION: US/09/933,115

TIME: 09:22:01

Input Set : A:\FISHERSEQLIST.TXT

Output Set: N:\CRF3\09102001\I933115.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:317 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:317 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:354 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:354 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:393 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:393 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11